using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

IN THE CLAIMS

Please amend claims 31 and 32 (a marked-up version showing changes made is attached hereto):

~~31.~~ (amended) An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide having calcium dependent protein kinase activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 90% identity based on the Clustal alignment method with multiple alignment default parameters of GAP PENALTY=10 and GAP LENGTH PENALTY=10 and pairwise alignment default parameters of KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5, or

(b) the complement of the nucleotide sequence.

~~32.~~ (amended) The polynucleotide of Claim ~~31~~, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method with the multiple alignment default parameters and the pairwise alignment default parameters.